SP 0 4 2001 SI

SEQUENCE LISTING

<110> Kato, Shigeaki Takeyama, Ken-Ichi Kitanaka, Sachiko

<120> GENE SCREENING METHOD USING NUCLEAR RECEPTOR

<130> 06501-054001

<140> 09/489,198

<141> 2000-01-20

<150> PCT/JP98/03280

<151> 1998-07-22

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<211> 507

<212> PRT

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Val Leu Arg Ser Leu Ser Asp Ile Pro Gly Pro Ser Thr Leu Ser Phe
35 40 45

Leu Ala Glu Leu Phe Cys Lys Gly Gly Leu Ser Arg Leu His Glu Leu 50 55 60

Gln Val His Gly Ala Ala Arg Tyr Gly Pro Ile Trp Ser Gly Ser Phe 65 70 75 80

Gly Thr Leu Arg Thr Val Tyr Val Ala Asp Pro Thr Leu Val Glu Gln 85 90 95

Leu Leu Arg Gln Glu Ser His Cys Pro Glu Arg Cys Ser Phe Ser Ser

Trp Ala Glu His Arg Arg Arg His Gln Arg Ala Cys Gly Leu Leu Thr 115 120 125

Ala Asp Gly Glu Glu Trp Gln Arg Leu Arg Ser Leu Leu Ala Pro Leu 130 135 140

Leu Leu Arg Pro Gln Ala Ala Gly Tyr Ala Gly Thr Leu Asp Asn 145 150 155 160

Val Val Arg Asp Leu Val Arg Arg Leu Arg Arg Gln Arg Gly Arg Gly
165 170 175

Ser Gly Leu Pro Gly Leu Val Leu Asp Val Ala Gly Glu Phe Tyr Lys 180 185 190

Phe Gly Leu Glu Ser Ile Gly Ala Val Leu Leu Gly Ser Arg Leu Gly 195 200 205

42

Cys Leu Glu Ala Glu Val Pro Pro Asp Thr Glu Thr Phe Ile His Ala 215 220 Val Gly Ser Val Phe Val Ser Thr Leu Leu Thr Met Ala Met Pro Asn 230 235 Trp Leu His His Leu Ile Pro Gly Pro Trp Ala Arg Leu Cys Arg Asp 245 250 Trp Asp Gln Met Phe Ala Phe Ala Gln Arg His Val Glu Leu Arg Glu 265 Gly Glu Ala Ala Met Arg Asn Gln Gly Lys Pro Glu Glu Asp Met Pro 280 285 Ser Gly His His Leu Thr His Phe Leu Phe Arg Glu Lys Val Ser Val 295 Gln Ser Ile Val Gly Asn Val Thr Glu Leu Leu Ala Gly Val Asp 310 315 Thr Val Ser Asn Thr Leu Ser Trp Thr Leu Tyr Glu Leu Ser Arg His 325 330 Pro Asp Val Gln Thr Ala Leu His Ser Glu Ile Thr Ala Gly Thr Arg 345 Gly Ser Cys Ala His Pro His Gly Thr Ala Leu Ser Gln Leu Pro Leu 360 Leu Lys Ala Val Ile Lys Glu Val Leu Arg Leu Tyr Pro Val Val Pro 375 380 Gly Asn Ser Arg Val Pro Asp Arg Asp Ile Arg Val Gly Asn Tyr Val 390 395 Ile Pro Gln Asp Thr Leu Val Ser Leu Cys His Tyr Ala Thr Ser Arg 405 410 Asp Pro Thr Gln Phe Pro Asp Pro Asn Ser Phe Asn Pro Ala Arg Trp 425 Leu Gly Glu Gly Pro Thr Pro His Pro Phe Ala Ser Leu Pro Phe Gly 435 440 445 Phe Gly Lys Arg Ser Cys Ile Gly Arg Arg Leu Ala Glu Leu Glu Leu 455 Gln Met Ala Leu Ser Gln Ile Leu Thr His Phe Glu Val Leu Pro Glu 470 475 Pro Gly Ala Leu Pro Ile Lys Pro Met Thr Arg Thr Val Leu Val Pro 485 490 Glu Arg Ser Ile Asn Leu Gln Phe Val Asp Arg 500 <210> 2 <211> 508 <212> PRT <213> Homo sapiens <400> 2 Met Thr Gln Thr Leu Lys Tyr Ala Ser Arg Val Phe His Arg Val Arg Trp Ala Pro Glu Leu Gly Ala Ser Leu Gly Tyr Arg Glu Tyr His Ser 25 Ala Arg Arg Ser Leu Ala Asp Ile Pro Gly Pro Ser Thr Pro Ser Phe 40

Leu Ala Glu Leu Phe Cys Lys Gly Gly Leu Ser Arg Leu His Glu Leu

Gln Val Gln Gly Ala Ala His Phe Gly Pro Val Trp Leu Ala Ser Phe

Gly Thr Val Arg Thr Val Tyr Val Ala Ala Pro Ala Leu Val Glu Glu

60

75

90

55

Cart a

Leu Leu Arg Gln Glu Gly Pro Arg Pro Glu Arg Cys Ser Phe Ser Pro 105 100 Trp Thr Glu His Arg Arg Cys Arg Gln Arg Ala Cys Gly Leu Leu Thr 120 Ala Glu Gly Glu Glu Trp Gln Arg Leu Arg Ser Leu Leu Ala Pro Leu 135 140 Leu Leu Arg Pro Gln Ala Ala Ala Arg Tyr Ala Gly Thr Leu Asn Asn 150 155 Val Val Cys Asp Leu Val Arg Arg Leu Arg Arg Gln Arg Gly Arg Gly 170 165 Thr Gly Pro Pro Ala Leu Val Arg Asp Val Ala Gly Glu Phe Tyr Lys 185 Phe Gly Leu Glu Gly Ile Ala Ala Val Leu Leu Gly Ser Arg Leu Gly 200 Cys Leu Glu Ala Gln Val Pro Pro Asp Thr Glu Thr Phe Ile Arg Ala 215 220 Val Gly Ser Val Phe Val Ser Thr Leu Leu Thr Met Ala Met Pro His 230 235 Trp Leu Arg His Leu Val Pro Gly Pro Trp Gly Arg Leu Cys Arg Asp 245 250 Trp Asp Gln Met Phe Ala Phe Ala Gln Arg His Val Glu Arg Arg Glu 265 Ala Glu Ala Ala Met Arg Asn Gly Gly Gln Pro Glu Lys Asp Leu Glu 280 285 Ser Gly Ala His Leu Thr His Phe Leu Phe Arg Glu Glu Leu Pro Ala 295 300 Gln Ser Ile Leu Gly Asn Val Thr Glu Leu Leu Ala Gly Val Asp 310 315 Thr Val Ser Asn Thr Leu Ser Trp Ala Leu Tyr Glu Leu Ser Arg His 330 325 Pro Glu Val Gln Thr Ala Leu His Ser Glu Ile Thr Ala Ala Leu Ser 340 345 Pro Gly Ser Ser Ala Tyr Pro Ser Ala Thr Val Leu Ser Gln Leu Pro 360 Leu Leu Lys Ala Val Val Lys Glu Val Leu Arg Leu Tyr Pro Val Val 375 380 Pro Gly Asn Ser Arg Val Pro Asp Lys Asp Ile His Val Gly Asp Tyr 390 395 Ile Ile Pro Lys Asn Thr Leu Val Thr Leu Cys His Tyr Ala Thr Ser 410 Arg Asp Pro Ala Gln Phe Pro Glu Pro Asn Ser Phe Arg Pro Ala Arg 420 425 Trp Leu Gly Glu Gly Pro Thr Pro His Pro Phe Ala Ser Leu Pro Phe 440 Gly Phe Gly Lys Arg Ser Cys Met Gly Arg Arg Leu Ala Glu Leu Glu 455 460 Leu Gln Met Ala Leu Ala Gln Ile Leu Thr His Phe Glu Val Gln Pro 470 475 Glu Pro Gly Ala Ala Pro Val Arg Pro Lys Thr Arg Thr Val Leu Val 485 490 Pro Glu Arg Ser Ile Asn Leu Gln Phe Leu Asp Arg

Chit

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ctg ggc tcc aga ggc agt gag tcg gtt ctc cgg agc ttg tct gac atc Leu Gly Ser Arg Gly Ser Glu Ser Val Leu Arg Ser Leu Ser Asp Ile 25 30 35 40	149							
cct ggg ccc tct aca ctc agc ttc ctg gct gaa ctc ttc tgc aaa ggg Pro Gly Pro Ser Thr Leu Ser Phe Leu Ala Glu Leu Phe Cys Lys Gly 45 50 55	197							
ggg ctg tcc agg ctg cat gaa ctg cag gtg cat ggc gct gcg cgg tac Gly Leu Ser Arg Leu His Glu Leu Gln Val His Gly Ala Ala Arg Tyr 60 65 70	245							
ggg cca ata tgg tct ggc agc ttt ggg aca ctt cgc aca gtt tac gtt Gly Pro Ile Trp Ser Gly Ser Phe Gly Thr Leu Arg Thr Val Tyr Val 75 80 85	293							
gcc gac cct aca ctt gtg gag cag ctc ctg cga caa gaa agt cac tgt Ala Asp Pro Thr Leu Val Glu Gln Leu Leu Arg Gln Glu Ser His Cys 90 95 100	341							
cca gag cgc tgt agt ttc tca tca tgg gca gag cac cgt cgc cgc cac Pro Glu Arg Cys Ser Phe Ser Ser Trp Ala Glu His Arg Arg Arg His 105 110 115 120	389							
cag cgt gct tgc gga ttg cta acg gcg gat ggt gaa gaa tgg cag agg Gln Arg Ala Cys Gly Leu Leu Thr Ala Asp Gly Glu Glu Trp Gln Arg 125 130 135	437							
ctc cga agt ctt ctg gcc ccg ctc ctc ctc cgg cca caa gca gcc gcg Leu Arg Ser Leu Leu Ala Pro Leu Leu Leu Arg Pro Gln Ala Ala 140 145 150	485							
ggc tat gct gga act ctg gac aac gtg gtc cgt gac ctt gtg cga cga Gly Tyr Ala Gly Thr Leu Asp Asn Val Val Arg Asp Leu Val Arg Arg 155 160 165	533							
cta agg cgc cag cgg gga cgt ggc tct ggg cta ccc ggc cta gtt ctg Leu Arg Arg Gln Arg Gly Arg Gly Ser Gly Leu Pro Gly Leu Val Leu 170 175 180	581							
gac gtg gca gga gag ttt tac aaa ttt ggc cta gaa agt ata ggc gcg Asp Val Ala Gly Glu Phe Tyr Lys Phe Gly Leu Glu Ser Ile Gly Ala 185 190 195 200	629							

CI Ci 2

			•												
					cgc Arg										677
					ata Ile										725
					atg Met										773
		-	_		tgc Cys	-	-		-	-	_		-	-	821
_					ctg Leu 270	_	_		_	-		_		_	869
					gat Asp										917
					gtg Val										965
			-	-	gga Gly		_	_	-			_			1013
					tcc Ser				-	_	-		_		1061
	Glu	Ile	Thr	Āla	ggg Gly 350	Thr	Arg	Gly	Ser	Cys	Ala				1109
					ctg Leu										1157
					gtg Val										1205
					aac Asn										1253
					act Thr										1301

CAL

•	
aac tot ttt aat coa got ogo tgg otg ggg gag ggt oog acc occ oac Asn Ser Phe Asn Pro Ala Arg Trp Leu Gly Glu Gly Pro Thr Pro His 425 430 435 440	1349
cca ttt gca tct ctt ccc ttc ggc ttt ggc aaa cgg agc tgc atc ggg Pro Phe Ala Ser Leu Pro Phe Gly Phe Gly Lys Arg Ser Cys Ile Gly 445 450 455	1397
aga cgc ttg gca gag ctt gag cta caa atg gct ttg tcc cag atc ttg Arg Arg Leu Ala Glu Leu Glu Leu Gln Met Ala Leu Ser Gln Ile Leu 460 465 470	1445
acc cat ttt gaa gtg cta cct gag cca ggt gct ctt cct atc aag ccc Thr His Phe Glu Val Leu Pro Glu Pro Gly Ala Leu Pro Ile Lys Pro 475 480 485	1493
atg acc cgg act gtc ctg gtc cct gag agg agc atc aat cta cag ttt Met Thr Arg Thr Val Leu Val Pro Glu Arg Ser Ile Asn Leu Gln Phe 490 495 500	1541
gta gat aga taaccattcg gaagacagcc aacatcgtct ctctcaagac Val Asp Arg 505	1590
aggatggggt ctttgttata cacaagaggc acactctcct tggaggcctg tctgaccgag caaactccag gaagcaggtc ctgacctatg tgtacttggc ctgactcage aggcatcgca gaaccaccat ctttctcctt cctgctcagt gcctctcctg atcattcctc aggatccaat gccttcagat tttaacacat ccttaaagtg ccaaacgcagg ggttaactac caactccagg cagcctgggg agggattcgc ccctgatcct gtagtgttcg ttgatgctct ttatcacggc acaagctaag tgattgcatc tggtctgcac tggtcgtac ctctacctga ccatgtgtgt gccttctgag aagagtaatg actagtctac tgggctttta gctctttttgagac agagtcttgc tatgtattcc atgctgctcc ggaaattcac aacttccttg cctcaccttt cccaagtatt gggttacaga cttgagctac cacttccagc tttatatcc ctgccagagt ctatcccttg gttattcag caccatacat ttctcagact gaacctggac catgtggcag gatcgccac tcaccaggct ctgccaccc ttttctctttatatctc ctctagggaa gtagtccac tcaccaggct ctgccaccc tttttctcttatatctc ctctagggaa gtaaatctgc ccttgcctaa tttacagcgt ttttaagcct ccctacctt ggttctcag gtaaatctgc ccttgcctaa tttacagcgt ttttaagcct ccctcacctt ggttctcag gtaaatctgc ccttgcctaa tttacagcgt ttttaagcct ccctcacctt ggttctcag gtaaatctgc ccttgcctaa tttcttatca tccatgttta ggcctgccct tctcca  <210> 4 <211> 2362 <212> DNA <221> misc_feature <222> (1)(1524) <221> misc_feature <222> (1)(2362) <223> n = A,T,C or G <<400> 4	1650 1710 1770 1830 1890 1950 2010 2070 2130 2250 2310 2370 2386
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CN+ C2

					_	ggc Gly	_					-					96
						gca Ala											144
						tgc Cys											192
	_		-		-	gcg Ala 70				_				_	_		240
						gtg Val											288
	_	_	_	_	-	gga Gly											336
						cgc Arg											384
_						tgg Trp											432
						gcg Ala 150											480
						gtg Val											528
						ctg Leu											576
						atc Ile											624
						gtg Val											672
			-			gtg Val 230		_	_	_		-		_			720
	tgg	ctg	cgc	cac	ctt	gtg	cct	ggg	ccc	tgg	ggc	cgc	ctc	tgc	cga	gac	768

ant a

					•											
Trp	Leu	Arg	His'	Leu 245	Val	Pro	Gly	Pro	Trp 250	Gly	Arg	Leu	Cys	Arg 255	Asp	
		cag Gln														816
-		gca Ala 275	_	-					_			_	-	_		864
		gcg Ala														912
		atc Ile														960
_		tcc Ser		_				-	_							1008
		gtc Val														1056
		tcc Ser 355														1104
_	-	aag Lys			_	_	-			_	_				-	1152
		aat Asn		-	-		-		-					_		1200
		ccc Pro														1248
	_	cct Pro	_	_								_		_	_	1296
		ggg Gly 435														1344
		ggc Gly	_	_	_	_	_		-		_	-				1392
_		atg Met	-	-	-	_								_		1440

Crxt C2

465	470	475	480
		acc cgg act gtc ctg Thr Arg Thr Val Leu 495	ı Val
	aac cta cag ttt ttg Asn Leu Gln Phe Leu 505		1534
aagaccaagg tatacatc agtgaagtgt gaggcggc	tt cccctaatgc ctatct tc tgaccaatgt gtgaag	aggg ataagatttt ttgt gacc aaactggata gaac tatg cacttggcct gact gccc ttctgatcat gtat	caccat 1654 caggaa 1714
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CZ.